1652 #12 DmJ 12249 OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/529,043A

DATE: 08/29/2001
TIME: 15:22:39

Input Set : A:\21437.ST25.txt
Output Set: N:\CRF3\08292001\I529043A.raw


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 5 <110> APPLICANT: Eikmanns, Bernd
 7       Peters-Wendisch, Petra
 9       Sahm, Hermann
13 <120> TITLE OF INVENTION: METHOD FOR MICROBIAL PRODUCTION OF AMINO ACIDS OF THE
ASPARTATE
14       AND/OR GLUTAMATE FAMILY
18 <130> FILE REFERENCE: 21437
22 <140> CURRENT APPLICATION NUMBER: 09/529,043A
24 <141> CURRENT FILING DATE: 2000-04-03
28 <160> NUMBER OF SEQ ID NOS: 2
32 <170> SOFTWARE: PatentIn version 3.0
36 <210> SEQ ID NO: 1
38 <211> LENGTH: 3728
40 <212> TYPE: DNA
42 <213> ORGANISM: Corynebacterium glutamicum
46 <400> SEQUENCE: 1
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51 ctatcaccct tggcggtctc ttgttgaaag gaataattac tctagtgtcg actcacacat    180
53 cttcaacgct tccagcattc aaaaagatct tggtagcaaa ccgcggcgaa atcgcggtcc    240
55 gtgctttccg tgcagcactc gaaaccggtg cagccacggt agctatttac ccccgtgaag    300
57 atcggggatc attccaccgc tcttttgctt ctgaagctgt ccgcattggt accgaaggct    360
59 caccagtcaa ggcgtacctg gacatcgatg aaattatcgg tgcagctaaa aaagttaaag    420
61 cagatgccat ttacccggga tacggcttcc tgtctgaaaa tgcccagctt gcccgcgagt    480
63 gtgcggaaaa cggcattact tttattggcc caaccccaga ggttcttgat ctcaccggtg    540
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67 ccccgagcaa aaacatcgat gagatcgtta aaagcgctga aggccagact taccccatct    660
69 ttgtgaaggc agttgccggt ggtggcggac gcggtatgcg ttttgttgct tcacctgatg    720
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73 cggtatatgt cgaacgtgct gtgattaacc ctcagcatat tgaagtgcag atccttggcg    840
75 atcacactgg agaagttgta caccttttatg aacgtgactg ctcactgcag cgtcgtcacc    900
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79 gtgcggatgc agtaaagttc tgccgctcca ttggttacca gggcgcggga accgtggaat   1020
81 tcttggtcga tgaaaagggc aaccacgtct tcatcgaaat gaacccacgt atccaggttg   1080
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87 cagcactgca gtgccgcatc accacggaag atccaaacaa cggcttccgc ccagataccg   1260
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91 agctcggtgg cgaaatcacc gcacactttg actccatgct ggtgaaaatg acctgccgtg   1380
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99 ctgatgatga gcagggacgc atcctggatt acttggcaga tgtcaccgtg aacaagcctc   1620
101 atggtgtgcg tccaaaggat gttgcagctc ctatcgataa gctgcctaac atcaaggatc  1680
103 tgccactgcc acgcggttcc cgtgaccgcc tgaagcagct tggcccagcc gcgtttgctc  1740
105 gtgatctccg tgagcaggac gcactggcag ttactgatac caccttccgc gatgcacacc  1800
107 agtctttgct tgcgacccga gtccgctcat tcgcactgaa gcctgcggca gaggccgtcg  1860
109 caaagctgac tcctgagctt ttgtccgtgg aggcctgggg cggcgcgacc tacgatgtgg  1920
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111 cgatgcgttt cctctttgag gatccgtggg acaggctcga cgagctgcgc gaggcgatgc 1980
113 cgaatgtaaa cattcagatg ctgcttcgcg gccgcaacac cgtgggatac accccgtacc 2040
115 cagactccgt ctgccgcgcg tttgttaagg aagctgccag ctccggcgtg gacatcttcc 2100
117 gcatcttcga cgcgcttaac gacgtctccc agatgcgtcc agcaatcgac gcagtcctgg 2160
119 agaccaacac cgcggtagcc gaggtggcta tggcttattc tggtgatctc tctgatccaa 2220
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125 agctggtcac cgcactgcgc cgtgaattcg atctgccagt gcacgtgcac acccacgaca 2400
127 ctgcgggtgg ccagctggca acctactttg ctgcagctca agctggtgca gatgctgttg 2460
129 acggtgcttc cgcaccactg tctggcacca cctcccagcc atccctgtct gccattgttg 2520
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157 agatccgccc aatgcgtgtg cgtgaccgct ccgttgagtc tgtcaccgca accgcagaaa 3360
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161 ctgttgctga aggtgatgag gtcaaggctg gagatgcagt cgcaatcatc gaggctatga 3480
163 agatggaagc aacaatcact gcttctgttg acggcaaaat cgatcgcgtt gtggttcctg 3540
165 ctgcaacgaa ggtggaaggt ggcgacttga tcgtcgtcgt ttcctaaacc tttctgtaaa 3600
167 aagccccgcg tcttcctcat ggaggaggcg gggcttttg ggccaagatg ggagatgggt 3660
169 gagttggatt tggtctgatt cgacactttt aagggcagag atttgaagat ggagaccaag 3720
171 gctcaaag 3728

174 <210> SEQ ID NO: 2
176 <211> LENGTH: 1140
178 <212> TYPE: PRT
180 <213> ORGANISM: Corynebacterium glutamicum
184 <400> SEQUENCE: 2
186 Met Ser Thr His Thr Ser Ser Thr Leu Pro Ala Phe Lys Lys Ile Leu
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189 Val Ala Asn Arg Gly Glu Ile Ala Val Arg Ala Phe Arg Ala Ala Leu
190 20 25 30
192 Glu Thr Gly Ala Ala Thr Val Ala Ile Tyr Pro Arg Glu Asp Arg Gly
193 35 40 45
195 Ser Phe His Arg Ser Phe Ala Ser Glu Ala Val Arg Ile Gly Thr Glu
196 50 55 60
198 Gly Ser Pro Val Lys Ala Tyr Leu Asp Ile Asp Glu Ile Ile Gly Ala
199 65 70 75 80
201 Ala Lys Lys Val Lys Ala Asp Ala Ile Tyr Pro Gly Tyr Gly Phe Leu
202 85 90 95
204 Ser Glu Asn Ala Gln Leu Ala Arg Glu Cys Ala Glu Asn Gly Ile Thr

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207 Phe Ile Gly Pro Thr Pro Glu Val Leu Asp Leu Thr Gly Asp Lys Ser
208         115                 120                 125
210 Arg Ala Val Thr Ala Ala Lys Lys Ala Gly Leu Pro Val Leu Ala Glu
211     130                 135                 140
213 Ser Thr Pro Ser Lys Asn Ile Asp Glu Ile Val Lys Ser Ala Glu Gly
214 145                 150                 155                 160
216 Gln Thr Tyr Pro Ile Phe Val Lys Ala Val Ala Gly Gly Gly Gly Arg
217                 165                 170                 175
219 Gly Met Arg Phe Val Ala Ser Pro Asp Glu Leu Arg Lys Leu Ala Thr
220             180                 185                 190
222 Glu Ala Ser Arg Glu Ala Glu Ala Ala Phe Gly Asp Gly Ala Val Tyr
223         195                 200                 205
225 Val Glu Arg Ala Val Ile Asn Pro Gln His Ile Glu Val Gln Ile Leu
226     210                 215                 220
228 Gly Asp His Thr Gly Glu Val Val His Leu Tyr Glu Arg Asp Cys Ser
229 225                 230                 235                 240
231 Leu Gln Arg Arg His Gln Lys Val Val Glu Ile Ala Pro Ala Gln His
232                 245                 250                 255
234 Leu Asp Pro Glu Leu Arg Asp Arg Ile Cys Ala Asp Ala Val Lys Phe
235             260                 265                 270
237 Cys Arg Ser Ile Gly Tyr Gln Gly Ala Gly Thr Val Glu Phe Leu Val
238         275                 280                 285
240 Asp Glu Lys Gly Asn His Val Phe Ile Glu Met Asn Pro Arg Ile Gln
241     290                 295                 300
243 Val Glu His Thr Val Thr Glu Glu Val Thr Glu Val Asp Leu Val Lys
244 305                 310                 315                 320
246 Ala Gln Met Arg Leu Ala Ala Gly Ala Thr Leu Lys Glu Leu Gly Leu
247                 325                 330                 335
249 Thr Gln Asp Lys Ile Lys Thr His Gly Ala Ala Leu Gln Cys Arg Ile
250             340                 345                 350
252 Thr Thr Glu Asp Pro Asn Asn Gly Phe Arg Pro Asp Thr Gly Thr Ile
253         355                 360                 365
255 Thr Ala Tyr Arg Ser Pro Gly Gly Ala Gly Val Arg Leu Asp Gly Ala
256     370                 375                 380
258 Ala Gln Leu Gly Gly Glu Ile Thr Ala His Phe Asp Ser Met Leu Val
259 385                 390                 395                 400
261 Lys Met Thr Cys Arg Gly Ser Asp Phe Glu Thr Ala Val Ala Arg Ala
262                 405                 410                 415
264 Gln Arg Ala Leu Ala Glu Phe Thr Val Ser Gly Val Ala Thr Asn Ile
265             420                 425                 430
267 Gly Phe Leu Arg Ala Leu Leu Arg Glu Glu Asp Phe Thr Ser Lys Arg
268         435                 440                 445
270 Ile Ala Thr Gly Phe Ile Ala Asp His Pro His Leu Leu Gln Ala Pro
271     450                 455                 460
273 Pro Ala Asp Asp Glu Gln Gly Arg Ile Leu Asp Tyr Leu Ala Asp Val
274 465                 470                 475                 480
276 Thr Val Asn Lys Pro His Gly Val Arg Pro Lys Asp Val Ala Ala Pro
277                 485                 490                 495
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```
279 Ile Asp Lys Leu Pro Asn Ile Lys Asp Leu Pro Leu Pro Arg Gly Ser
280             500                 505                 510
282 Arg Asp Arg Leu Lys Gln Leu Gly Pro Ala Ala Phe Ala Arg Asp Leu
283         515                 520                 525
285 Arg Glu Gln Asp Ala Leu Ala Val Thr Asp Thr Thr Phe Arg Asp Ala
286     530                 535                 540
288 His Gln Ser Leu Leu Ala Thr Arg Val Arg Ser Phe Ala Leu Lys Pro
289 545                 550                 555                 560
291 Ala Ala Glu Ala Val Ala Lys Leu Thr Pro Glu Leu Leu Ser Val Glu
292                 565                 570                 575
294 Ala Trp Gly Gly Ala Thr Tyr Asp Val Ala Met Arg Phe Leu Phe Glu
295             580                 585                 590
297 Asp Pro Trp Asp Arg Leu Asp Glu Leu Arg Glu Ala Met Pro Asn Val
298         595                 600                 605
300 Asn Ile Gln Met Leu Leu Arg Gly Arg Asn Thr Val Gly Tyr Thr Pro
301     610                 615                 620
303 Tyr Pro Asp Ser Val Cys Arg Ala Phe Val Lys Glu Ala Ala Ser Ser
304 625                 630                 635                 640
306 Gly Val Asp Ile Phe Arg Ile Phe Asp Ala Leu Asn Asp Val Ser Gln
307                 645                 650                 655
309 Met Arg Pro Ala Ile Asp Ala Val Leu Glu Thr Asn Thr Ala Val Ala
310             660                 665                 670
312 Glu Val Ala Met Ala Tyr Ser Gly Asp Leu Ser Asp Pro Asn Glu Lys
313         675                 680                 685
315 Leu Tyr Thr Leu Asp Tyr Tyr Leu Lys Met Ala Glu Glu Ile Val Lys
316     690                 695                 700
318 Ser Gly Ala His Ile Leu Ala Ile Lys Asp Met Ala Gly Leu Leu Arg
319 705                 710                 715                 720
321 Pro Ala Ala Val Thr Lys Leu Val Thr Ala Leu Arg Arg Glu Phe Asp
322                 725                 730                 735
324 Leu Pro Val His Val His Thr His Asp Thr Ala Gly Gly Gln Leu Ala
325             740                 745                 750
327 Thr Tyr Phe Ala Ala Ala Gln Ala Gly Ala Asp Ala Val Asp Gly Ala
328         755                 760                 765
330 Ser Ala Pro Leu Ser Gly Thr Thr Ser Gln Pro Ser Leu Ser Ala Ile
331     770                 775                 780
333 Val Ala Ala Phe Ala His Thr Arg Arg Asp Thr Gly Leu Ser Leu Glu
334 785                 790                 795                 800
336 Ala Val Ser Asp Leu Glu Pro Tyr Trp Glu Ala Val Arg Gly Leu Tyr
337                 805                 810                 815
339 Leu Pro Phe Glu Ser Gly Thr Pro Gly Pro Thr Gly Arg Val Tyr Arg
340             820                 825                 830
342 His Glu Ile Pro Gly Gly Gln Leu Ser Asn Leu Arg Ala Gln Ala Thr
343         835                 840                 845
345 Ala Leu Gly Leu Ala Asp Arg Phe Glu Leu Ile Glu Asp Asn Tyr Ala
346     850                 855                 860
348 Ala Val Asn Glu Met Leu Gly Arg Pro Thr Lys Val Thr Pro Ser Ser
349 865                 870                 875                 880
351 Lys Val Val Gly Asp Leu Ala Leu His Leu Val Gly Ala Gly Val Asp
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352                 885                 890                 895
354 Pro Ala Asp Phe Ala Ala Asp Pro Gln Lys Tyr Asp Ile Pro Asp Ser
355             900                 905                 910
357 Val Ile Ala Phe Leu Arg Gly Glu Leu Gly Asn Pro Pro Gly Gly Trp
358         915                 920                 925
360 Pro Glu Pro Leu Arg Thr Arg Ala Leu Glu Gly Arg Ser Glu Gly Lys
361     930                 935                 940
363 Ala Pro Leu Thr Glu Val Pro Glu Glu Glu Gln Ala His Leu Asp Ala
364 945                 950                 955                 960
366 Asp Asp Ser Lys Glu Arg Arg Asn Ser Leu Asn Arg Leu Leu Phe Pro
367                 965                 970                 975
369 Lys Pro Thr Glu Glu Phe Leu Glu His Arg Arg Arg Phe Gly Asn Thr
370             980                 985                 990
372 Ser Ala Leu Asp Asp Arg Glu Phe  Phe Tyr Gly Leu Val  Glu Gly Arg
373         995                 1000                1005
375 Glu Thr  Leu Ile Arg Leu Pro  Asp Val Arg Thr Pro  Leu Leu Val
376     1010                1015                1020
378 Arg Leu  Asp Ala Ile Ser Glu  Pro Asp Asp Lys Gly  Met Arg Asn
379     1025                1030                1035
381 Val Val  Ala Asn Val Asn Gly  Gln Ile Arg Pro Met  Arg Val Arg
382     1040                1045                1050
384 Asp Arg  Ser Val Glu Ser Val  Thr Ala Thr Ala Glu  Lys Ala Asp
385     1055                1060                1065
387 Ser Ser  Asn Lys Gly His Val  Ala Ala Pro Phe Ala  Gly Val Val
388     1070                1075                1080
390 Thr Val  Thr Val Ala Glu Gly  Asp Glu Val Lys Ala  Gly Asp Ala
391     1085                1090                1095
393 Val Ala  Ile Ile Glu Ala Met  Lys Met Glu Ala Thr  Ile Thr Ala
394     1100                1105                1110
396 Ser Val  Asp Gly Lys Ile Asp  Arg Val Val Val Pro  Ala Ala Thr
397     1115                1120                1125
399 Lys Val  Glu Gly Gly Asp Leu  Ile Val Val Val Ser
400     1130                1135                1140
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